

SEQUENCE LISTING

<110> Pfizer Inc

<120> Novel Polypeptide

<130> PC10914ADAM

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<141>

<150> 0008504.3

<151> 2000-04-05

<150> 60/198,367

<151> 2000-04-19

<160> 6

<170> PatentIn Ver. 2.0

<210> 1

<211> 993

<212> DNA

<213> Homo sapiens

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gggttGtcca tatAtGttt CCTGcAGCCT tataAGAAgt ccACAtCTgt gAACGtttC 180

atgctAAAtC tggccATTtC agAtCTCCTG ttcAtAAGCA CGtTCCtT cAgGgCtGAc 240

tattAtCTtA gaggCtCCAA ttggAtAttt ggAGACtGG CCTGcAGGAt tAtGtCttAt 300

tccttGtAtG tcaACAtGtA cAGCAGtAtt tAttCCTGA CCgtGtGAG tGtGtGcgt 360

ttcctGgcaa tggttcacCC ctttcggCtt ctGcatgtCA ccAGcatcAG gagtgCtGg 420

.AtcctctgtG ggAtcatAtG gAtccttAtC AtggCttCt caAtAAtGtC cctggacAGt 480

ggctctGAGC agAACGGCAG tGtCACAtCA tGcttagAGC tGAAtCtcta tAAAAttGtC 540

aAGtGcAGA ccatGAActA tattGcCttG gtggGggCt gcctGtGcc AttttCaca 600

ctcAGcatct gttAtCtGtCt gAtcattCgg gttCtGttaA aAGtGgAGgt cccAGAAtCg 660

gggctcgaaa tttctcacag gaaggcactg accaccatca tcatacacctt gatcatcttc 720
ttcttggtt tcctgcctta tcacacactg aggaccgtcc acttgacgac atggaaagtg 780
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 Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu
 35 40 45
 Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu
 50 55 60
 Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp
 65 70 75 80
 Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg
 85 90 95
 Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe
 100 105 110
 Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe
 115 120 125
 Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly
 130 135 140
 Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser

145	150	155	160
Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu			
165	170	175	
Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val			
180	185	190	
Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile			
195	200	205	
Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val			
210	215	220	
Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe			
225	230	235	240
Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr			
245	250	255	
Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val			
260	265	270	
Ile Thr Leu Ala Leu Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu			
275	280	285	
Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu			
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Ser Val Trp Leu Arg Lys Glu Thr Arg Val			
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Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr
20 25 30

att gaa aac ttc aag aga gaa ttt ttc cca att gta tat ctg ata ata 144
Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile
35 40 45

ttt ttc tgg gga gtc ttg gga aat ggg ttg tcc ata tat gtt ttc ctg 192
Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu
50 55 60

cag cct tat aag aag tcc aca tct gtg aac gtt ttc atg cta aat ctg 240
Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu
65 70 75 80

gcc att tca gat ctc ctg ttc ata agc acg ctt ccc ttc agg gct gac 288
Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp
85 90 95

tat tat ctt aga ggc tcc aat tgg ata ttt gga gac ctg gcc tgc agg 336
Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg
100 105 110

att atg tct tat tcc ttg tat gtc aac atg tac agc agt att tat ttc 384
Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe
115 120 125

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Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe		
130	135	140
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Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly		
145	150	155
atc ata tgg atc ctt atc atg gct tcc tca ata atg ctc ctg gac agt		528
Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser		
165	170	175
ggc tct gag cag aac ggc agt gtc aca tca tgc tta gag ctg aat ctc		576
Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu		
180	185	190
tat aaa att gct aag ctg cag acc atg aac tat att gcc ttg gtg gtg		624
Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val		
195	200	205
ggc tgc ctg ctg cca ttt ttc aca ctc agc atc tgt tat ctg ctg atc		672
Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile		
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Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val		
225	230	235
240		
tct cac agg aag gca ctg acc acc atc atc acc ttg atc atc ttc		768
Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe		
245	250	255
ttc ttg tgt ttc ctg ccc tat cac aca ctg agg acc gtc cac ttg acg		816
Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr		
260	265	270
aca tgg aaa gtg ggt tta tgc aaa gac aga ctg cat aaa gct ttg gtt		864
Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val		
275	280	285
atc aca ctg gcc ttg gca gca gcc aat gcc tgc ttc aat cct ctg ctc		912
Ile Thr Leu Ala Leu Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu		
290	295	300
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Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu		
305	310	315
		320

aga aaa ggc cat cca aag aag gca aac aac aac tgg gtt ttccact gtt 1008
Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val
325 330 335

agt gtg tgg ttg aga aag gaa aca aga gta taa 1041
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<212> PRT
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20 25 30

Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile
35 40 45

Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu
50 55 60

Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu
65 70 75 80

Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp
85 90 95

Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg
100 105 110

Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe
115 120 125

Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe
130 135 140

Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly
145 150 155 160

Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser
165 170 175

Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu
180 185 190

Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val
195 200 205

Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile
210 215 220

Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val
225 230 235 240

Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe
245 250 255

Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr
260 265 270

Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val
275 280 285

Ile Thr Leu Ala Leu Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu
290 295 300

Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu
305 310 315 320

Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val
325 330 335

Ser Val Trp Leu Arg Lys Glu Thr Arg Val
340 345